

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number:

TO: Terra Gibbs

Location: CM1/12A12/11E12

Art Unit: 1635

Tuesday, June 24, 2003

Case Serial Number: 998667

From: Mary Jane Ruhl

**Location: Biotech-Chem Library** 

CM1-6A06

Phone: 605-1155

maryjane.ruhl@uspto.gov

Search Notes	



From:

Gibbs, Terra

Sent:

Wednesday, June 18, 2003 12:46 PM

To: Subject: STIC-Biotech/ChemLib Sequence search request...

Could you please do a regular search of SEQ ID NO: 2 of USSN 09/998667?

Thank You!

Terra Gibbs AU 1635 306-3221

Mailbox: 11E12

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Tech. Info. Specialist, STIC TC-1600 CM-1, Room 6A-06

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Minimum DB seq length: 0
Maximum DB seq length 200000000
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Pred. No is the number of results predicted by charge to have

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#### ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	POCUS	RESULT 1 AK000463
<pre>"</pre>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoctomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	Homo sapiens signet-ring cell carcinoma cell_line:KATC III cDNA to mRNA, clone lib:KAT clone:KATG5827.	oligo capping; fis (full insert sequence).	AK000463 1 GI-7020568	AK000463	Homo sapiens cDNA FLJ20456 fis, clone KAT05827.	AK000463 1916 bp mRNA linear PFI 22-FEB 2000	

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Villalon.D K , Luna, P.A. Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Hölloway, M., Telford, B, Hodgson, A. Bouck, J. Yu, W.,
Muzny,D.M., Gibbs,R.A.
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Submitted (30 UM, 2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Camoer Genomics Office, National Camoer
Institute, 31 Center Drive, Page 11AC3, Fethesda, ME 20892-2590,
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/organism."Homo sapiens"
/db xref "taxon.9606"
/il.ue-"M30.13131 IMA3E.4521247"
/tissue type-"Testis, embryonai dardinoma"
/clone_Tib="NIH_MGC_92"
                                                                                                                      Location/Qualifiers
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                                                                                                                                            AGTCTTAGACCGGTCACTTCTTGAATATGTGAATCACTCGAACACAGCATAATTTTATTA 7.0
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                       AGGGAAGTTGTCAATGATTGATGGGGCAAAAATGTACAACACACTTATGTGTTTTTCTCCATG 1824
                                                                                                   AAACGAAGGGAAAAGGGACCACTGAATTGCACCATTTAAGATGCTGCTTGAACAAATTTG
                                                                                                                                                                                  AGTOTTAGACOGGICACTICTTGAATAIGIGAATCACTCGAACACCACATAA.TTTATTA 1214
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/preduct."Uthrown (protein for MGC:21737)"
/protein_id="AAH12021.1"
/protein_id="AAH12021.1"
/protein_id="AGH1208USTDSGKSAPASATARALERRRDPELPVTSFDCAVCLEVL
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#GPVPTPP-HVF-PS-1ATSLFHNEWT-TY-FAYLES-TV-FAYUS-SELLETTTH
GDIVLYLSEMPAHIRTOGKYIDKYGPUGELEETAAFCVCPFFQFELYEUS-SLLIHTTH
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dligo dapping: fis (full insert sequence).
Madada fascioularis adult male temporal lobe right cDNA to mERA,
clone_lib:macaque_brain cDNA library QtrA clone:QtrA-14722.
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Mataed faceltalyris train tONA olone-OtrA 14702, full insert
Hasshimoto, F., Osada, N., Hida, M.,
                                                                                   Osada, M., Hida, M., Kusuda, T., Tanuma, P., Tseki, K., Hirai, M., Terao, K., Subuki, Y., Sugaro, S. and Hashimoto, K.
Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                      Madada fascicularis
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Frimates; Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                       sequence
                                        Unpublished
                                                                                                                                                                         Cercopithecinae; Macaca
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      Kusuda, J. and Sugano, S
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                                                                                                                                                                                                                                                                                                                                                                                              459 ACTGAGTGCTTCGCAGCTGTCTCAGAGAGAGAGACAAAGAGACAAAGAGACC
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R Site2: DraIII (CACTGTGTG)

Description lat strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments <1.5kb.The Sfil-digested PCR product was coloned into distinct DraIII sites of pMEJ85-F13. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method [Sugano et al., Institute of Mcdical Science, University of Tokyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (27 APP-2001) Katsuyuki Hashimoro, National Institute of Infectious Disease, Division of Genetic Resources, 23 1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (S-mail-khashiknih gc jp. UFC http://www.cil.gc.jp/y-ken/g-n-Fark/Tel.81-3-5285 1111(ex.2120), Fax:81 3 5285 1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Custom primer used for sequencing (5' end primer [CTTCTGCTCTAAAAGCTGCG]; 'end primer [CGACCTGCAGCTCGAGCACA]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lab host:
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                                                                                                              AACAAGTOGACCTGTCCTTA ITOGCOSSGCATATCTTCCCIGAGAA SGACTTCCAGCAACT
                                                                                                                                                                                                STOOGGACCCCCTGOGGCCACCTATTCTGCCGTTCTGTGATTACTACCACTGGAAGAAC
                                                                                                                                                                                                                                                                                                                                                                            GATGTAGCCAAAAGAATGAAATCAGAGTATAAGAACTGCAMMGAGTGTGACACCCTGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="temporal lobe right"
/clone_Tib="macaque brain cDNA library CtrA"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
/protein_id="BAB46910.1"
/db_xref="GI:13874603"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="QtrA-14722"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9541"
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DraIII (CACTGTGTG)
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/W95W1TTP999W39CT5W39C 17 	790193011A05711 	N -4	
BAAAATTTTGGAAGTCAAGAAAGT 17 	ATCTTSTATSGSASTTGSAAAG           ATCTTSTACRRAGTTGSAAAG	→ €	
TGCCCTTGCTCTAATCTCTAATA 18	AUTOCASJACATTERAAJSAAATAASAAATOTSETECAA 	1599 1137	
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TGCTACATATCAATAACTACCAT 15                          TACTACATATTAATAACTACCAT 10	ATCTCGGTTTGCAAATTAGATAATACTCTGTGTGTATA	1479 1619	
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TACACATOTTAACAAGAAAAAA 14                 TACACATOTAACAAAAAAA 95	TTTTAATGGTTTAAAT-TGTTTTA-TATCCTSA-	1359 901	
TASTSCATTTAAAAANSSCTTTAA 148 	A "WA "ACASTTATSPRITESTO"A DOLTATION	1299 841	
AATSATTSATSSSCAAAAATST 12 	TITAAGATGITGITTGAAFAAATGGGAGGGAAGFIGI 	1239 781	
AGGGACTACT          AGGGACCACT	CROTOGRACACOROATRATTTTATTANANO 	127	
DOACTTOTTGAATATGTGAAT 1 	ATAATTGAGGAAGCTCTTATCCGA 	1119	
BATGATTTÇATAGA              BATGATTTÇATAGA	TTAATAASACATCTSTAASTTASTCACACT	1059	
CAAGCAG           CAAGCAG	GROTTCTSTCCACTITISCOSTITAATACCC	999 541	
TCACAG         TCACAG	CHGRATGAGSACASCTESTESTATCATTSTATTACE	919 481	
STATGTCCCTTTTGTCAGAGGGAA 93 	CCACTACAAGAACTTGAGGAGAGAGGAGGAGGTGTG 	879 421	
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1959 GCTGAGATOGOGCCAGTACACTCCAGCCTGGGTAAACAGAGCTAGACTCCATCTCAAAAAA 2018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-AUG-1999) Whitehead Institute/MIT Center for Genome research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 24, 2000 this sequence version replaced gi:5732131.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp-gen.ge.waschingtr.edu/FM.FepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPROXIMENT FROM PART FOR AMPLE OF THAT FIG 24-MAP-2000 Homo sapiens chromosome 18 clone RP11-5316 map 18, WCFKING DPAFT SECURIOR. 16 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                        Consensus quality: 151692 bases at least Q40 Consensus quality: 157600 bases at least Q30 Consensus quality: 159905 hases at least Q20 Insert size: 192000; agarose-fp Insert size: 164718; sum-of-contigs Quality coverage: 4.7 in Q20 bases; agarose-fp quality coverage: 4.2 in Q20 bases.
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                                                                                                                                                                                                                                                                                            Center clone name: 53_16

Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-primer-amersham; 27% of reads
Chemistry: Dye-terminator Big Dye; 73% of reads
Chemistry: Dye-terminator Big Dye; 73% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seg.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       project name: L1292
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draft' sequence. It currently The true order of the pieces
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38073 38172; conti
38173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38073 38172. gap of 100 kp 38173 47433; contig of 9261 bp in length 47434 47533; gap of 100 bp 100 bp in length 47534 54692; contig of 7159 bp in length 54693 54792, gap of 100 bp 54793 69069; contig of 14277 bp in length
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124646 166218: contig of 41573 bp in length
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19207 25620; contig of 6414 bp in length
25621 25720; gap of 100 bp
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10487 15318: contid of 4832 bp in length
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82605: contig of 13436 bp in length
705: gap of 100 bg
95840 contig of 13185 bp in length
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19106: contig of 3688 bp in length
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31795: contig of 6075 bp in length
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Harna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Chararata, J., Chararo, B., Chopel, Y., Collymore, A., Cook, A. Cooke, P., Pearellano, K., Dewar, K., Diaz, J.S., Podge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Cord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
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Mammalia: Eurheria, Primates, Catarrhini, Hominidae, Homo.
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Birren,B., Nusbaum,C. and Lander,E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (ns. HT -2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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Horton, L., Hulme, W., Iliev, I., Jihnsin, E., Jihos, T., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad Toh, K., Liu, G., Mailbeat, C., Majorall, F., Majory, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Wirphy, T., Maylot, J., Myuyet, C., Mill, E., Mill, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Pervison, K., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Pervison, K., Raymond, C., Retta, R., Rise, C., Koyov, P., Phinkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Koyov, P., Poman, J., Poy, A., Schauer, S., Schupback, P., Scaman, S., Fryoty, P., Smith, C., Spencer, B., Stange Thomann, N., Stofjanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Tarvers, M., Vassni, V., H., Vill, P., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zairoun, D., Stember, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (1) (IL-1982) Whitehead Institute/MIT Center for Genome Research, 1. harles street, Jankridge, MA 12141, USA on Jul 13, 1282 this sequence version replaced gi:21699449.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
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Center code: WIBR
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                        /rpt_family="AluSq"
Complement(7052...7105)
/note_"single_clone_coverage"
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complement(2974, .3)
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Overy Match 44.4%, Score 900.8, DB 9, Length 176222;
Boot Local Similarity 95.7%, Prod. No. 29.203;
Matches Jio, Conservative 0, Mismatches 42, Indels 0, Gaps
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                                                            /rpt_family="L2"
complement(20598..20658)
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complement(1/259, 1849)
/rpt family="AluSx"
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complement(10349 10651)
/rpt_family="AluSc"
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9306. .9330
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/rpt_family="AluSq"
complement(13440...13580)
/rpt_family="L2"
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complement(8993.
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complement(15744
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10877. .11173
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14987, .15295
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Tement(14037. .14344)
family="THE1C"
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Tement(15989.
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AC636167 AC636167 PMA linear HTG 25 JUN 2000 Homo sapiens chromosome 18 clone RP11 592123 map 18, WOPKING DPART SEQUENCE, 43 unordered pieces.

1064 AAGACATCTGCAAGTTAGTCACACTTTGTTTTATGATGATTTCATAGATTTTAATAATAAT 1123

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Smit. A.F.A. & Green, P. (1996-1997)
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Consensus quality: 15738 bases at least Q30 Consensus quality: 169108 bases at least Q30 Consensus quality: 174071 bases at least Q20 Consensus quality: 174071 bases at least Q20 Insert size: 207000; significantly consensus quality: 174071 bases at least Q20 Insert size: 207000; significantly consensus quality: 174070 significantly consensu
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SOURCE ORGANISM VERSION DEFINITION AC009831 KEYWORDS Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo, 1 (bases 1 to 179409)

Birren, B., Misbaum, C., and Lander, E. Homo sapiens

HTG AC009831.21 Homo sapiens chromosome , clone RP11-326K13, complete human AC009831 AC009831 GI:22038645 179409 bp DNA linear PRI 01-AUG-2002 ecunence

Unpublished Homo sapiens chromosome, clone RP11-326K13

Birrel, B., Linton, L., Mushaum, C., Lindor, E., Allon, M., Anderson Baker, J., Baldwin, J., Barna, M., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Devar, K., Doncelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., (bases 1 to 179409)

Anderson, M

REFERENCE

AUTHORS

JOURNAL

TITLE

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RS. Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, M., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Collins, S., Collins, S., Collins, S., Collymore, A., Chazaro, B., Choeppl, Y., Colangelo, M., Collins, S., Collymore, A., Chazaro, B., Choeppl, Y., Colangelo, M., Collins, S., Collymore, A., Collins, S., Collins, S., Collymore, A., Collins, S., Collins, S., Collins, S., Collins, S., Collins, C., Macolonald, P., Major, J., Levine, R., Lindblad-Toh, K., Linu, G., Marchan, C., Macolonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meddrim, J., Marchan, C., Macolonald, P., Major, J., Naylor, J., Nguyen, C., McCarthy, M., McEwan, P., McKernan, K., Meddrim, J., Woonnell, P., Collins, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Pollara, V., Poserri, M., Poy, A., Santos, P., Schaiper, S., Schupback, P., Schaiper, S., Chabler, S., Charles, M., Strange-Thomann, N., Strange, T., Collins, M., Strange, C., McCarthy, M., Strange, P., Schaiper, S., Strange, C., McCarthy, M., Strange, P., Schaiper, S., McCarthy, M., Strange, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Airam, A. Nusbaum, C. Lander, E., Ali, A., Allen, N., Anderson, S., Barram, N., Bastien, V., Bloom, T., Boguslavity, L., Boukhgalter, B., Conk, A., Chang, J., Chararo, B., Choepel, Y., Collymore, A., Conk, A., Choke, P., DeArellann, K., Dewar, K., Diaz, J. S., Dodge, S., Fairo, S., Feirella, P., Firzberild, M., Sage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Graham, L., Graham, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kararas, A., Kells, C., Landers, T., Levine, D., Lindblad-Toh, K., Liu, G., Marthews, C., Landers, T., Levine, J., Marthews, C., McCarthy, M., Meldrim, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Mayler, T., Myles, C., Misch, E., Miker, C., Merman, C.H., O'Connort, J., Johnson, L., Mihova, T., Mlenga, V., Murphy, T., Myler, T., Myles, C., Misch, P., Misch, P., Peterson, K., Phunkhang, P., Piarre, N., Paymond, P., Peter, P., Fise, C., Fogov, P., Smirh, C., Spennet, E., Schupback, R., Seaman, S., Severy, P., Smirh, C., Spennet, E., Stanger, Thomann, N., Stanger, N., Talamas, J., Viel, R., Vo, A., Wison, R., Wu, X., Wyman, D., Young, S., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Research, 320 Charles Street, Cambridge, MA 02141, USA of Any 1, 202 this sequence version replaced gi 21327831 All repeats were identified using RepeatMasker Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp-genome.washington.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
Contral sequence submissions@en.me.wi.mit.edu
Project Information
Center clone name: 12384
Center clone name: 124_K_II
                                                                                                                                                                                                                                                                                                        Center code: WIBR
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AUTHORS
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                                                                                                                                                     RESULT 8
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                                                                   KEYWORDS
                                                                                                                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                      AL162596 FMA sequence from Clone RE1 19820 on
        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutricostomi;
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 116067)
                                            Homo sapiens
                                                                                                     complete sequence.
                                                       human.
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/clone=lib="PPCT-11 Human Male PAC"
, 28542 > 3852P g soong t
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99.7%;
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Pred. No. 8.4e-145;
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115084 ATSAAAGGCTGAAAATTAATGATCTAATACAGGAAAGTGGAATTAAAAAAATAATGCTAA 115628
                                                                                                                                                                                                                                                                                    115744 GATATACAGAAAAAGCAATAAAAGTAAGGAGAATTAAGACTTTAAAAGTTTATATAAAAT 115685
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                               1652 TCTAATAGGTTAACGTTAATAATCTTGTATGGGAGTTGGAAAGGAAAATTTTGGAAGTCA 1711
                                                                                                                                                                                                                                                                                                                                                  1592 SAWACANASTSCAGACATTCAAAGAAATAAGAAATCTGCTCCAATGCTCTTGTTCTAATC 1651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Oct 25, 2001 this sequence version replaced gi:15858887. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission cirroseconing is the overlapping clone, as we submit sequences with only a small overlap as described above.
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Submirted (24 OTT 2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 18A, UK E-mail enquiries humquery@sanger ac.uk Clone
requests clonerequest@sanger ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
RP1-13P20 is from the library RPCI-1 constructed by the group of Pieter de 3:13. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ad.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RP1-13P20 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RP1-13P20 is at 116067 in this sequence. The true left end of clone RP1-20N18 is at 106583 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VECTOR: prypar2
IMPORTANT: This sequence is not the entire insert of clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence. The true right end of clone RP1-43017 is at 2000 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www_chori_org/bacpac/home_htm
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/more="Sequence from overlapping clone RP1-20N18:
(AL356867). Assembly confirmed by restriction digest."
1 23814 c 23805 g 33832 t
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restriction digest data."
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                                                                                                                                                                                                                                                                                                                                                                                                                        11.4%, Score 232.2, DB 9, 73.7%; Fred. No. 3.9e-44; tive 0; Mismatches 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= no); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M1% subclone; and the assembly was confirmed by restriction digest. The following abserviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, WMSSFPOT; Tr., TPEMBL; Wp:, WCFMFEF; Information of the WCRMPEF database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL356867 14780% bp CNA linear PRI 12 FEB 200
Human DNA sequence from clone RPI 20N18 on chromosome 1, complete
RPI 20N18 It may be shorter because we sequence everlapping sections only once, except for a short overlap. The true right end of clone RPI-20N18 is at 147803 in this sequence. The true left end of clone RPI-59H12 is at 107462 in this sequence. The true right end of clone RPI-59H12 is at 107462 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sangor.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger ac.uk Clone requests: olonerequest@sanger ac.uk
on Feb 13, 2002 this sequence version replaced gi:16304649.
                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/HGP/Chrl
RPI-20N18 is from the library RPCI-1 constructed by the group of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 During sequence assembly data is compared from overlapping clones Where differences are found these are annotated as variations
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database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         corresponding to the overlapping clone, as we submit sequences with
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                                                                                                                                                                                                                                                                                                             Pieter de Jong. For further details see
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Direct Submission
Chheire 3 (13 MAY 1949) Masahira Hattori, The Institute of Physical and Oberical Pesearch (PIYEN), Genemic Sciences Center (SSC); Kirasato Univ., 1-15 1 Mitscaro, Sagamihara, Managawa 228-8555, Japan (E-mail:hattorisgsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APCODES | APCODE
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2 (bases 1 to 10000)

Hattwink, Ishirk, Tyrk, A. Th. Part and Gakaki, Y. Direct Submission
Submitted (11-MAY-1998) Masslira Hatt-11, Effactory Efficatory, Speciationer of Science, JST Sequencing Laboratory, Effactor (15-1), Sagamihara 228, Japan (E-mail-hattoring Caloristic tokyolasi, profile (16-27-78-9732, Fax:0427-78-9561)

This sequence is Frank, the first Hilbert tyre organization as a Unit of Sequencing team.
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The sequence is a part of the data (ACCESSION No. APOCCIC)
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Eukaryota, M
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Sub leader: Tadayoshi Shiba Ph D , Masahira Hattori Ph.D. The
Sequence is submitted by:Human Genome Sequencing in ALIS project of
                           Direct Submission
Submitted (10 MAY 1999) Masahira Hattori
                                                                                                           Harrori,M., Ishii,K., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
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Homo sapions 1,100,202bg genomic DNA of 21q22.1 (REGION: D21S226-AMI, CLONE PANGE: f43D11-11988)
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and Chemical Research (RIKEN), Genomic Sciences Center (GSC)
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                                Hirakawa M ,
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Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                       Homo sapiens (human)
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Location/Qualifiers
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Japan (E mail:hattoriwgsc riken go jp,
URL.http://hopp.gsc.viken.go.jp/, Tel:81 42-778 9923,
Fax:81-42-778-9924)
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6.1, Yorkharch, Chiyeda-ku, Tokyo 122-0881 Japan
For further information about this sequence, including its
location and relationship to other sequences, please visit our
sequence archive Web site (http://www.alis.tokyo.jst.go.jp/HGS/)
or send email to webmasterxwww-alis.tokyo.jst.go.jp
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Principal Investigator-Yoshiyuki sakaki Ph P
Phone: +81-1-5449-5622, Fax - +81-3-5449-5445,
sababiuhgo imm u-rokyo ac jp
Sub-leader- Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D.
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                                                                                                                    * Ihnestrasse 73, D-14195 Berlin, Ger

* e.mail. info-chr21amdjgen.mpg.de

* UpL hetp //-br21 vz berlin.mpg de/

Alle3256: Submitted (10 Apr-2000).
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Beutenbergstrasse 11, D-07745 Jena, Germany,
* e mail: gscj-submitigenome imb-jena de
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Humo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * e.mail: nshimizu@dmb-med.keio.ac.jp
                                                                                                                                                                                                                                                                                                                                                                             GEF, Dept. of Genome Analysis, Mascheroder Weg 1, D-38124 Braunschweig, Germany, • • .mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                URL: http://www.dmb.med.keio.ac
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                                                                                                                                                                                                                                                     Max-Planck Institute for Molecular Genetics,
                                                                                                                                                                                                                                                                                                               URL: http://genome.gbf.de/
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Submitted (16-MAR-2001) Masahira Hattori. The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1 7-22 Subhiro Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriagar Tivon go jr. Unit http://hgg-gs-rivon-go-jr/.
Tel:81-45-503-9111, Fax:81-45-503-9970)
On Aug 9, 2002 this sequence version replaced gi:13383332.
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GenCore version 5.1.6 Copyright (c) 1993 2003 Compugen Ltd.

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#### ALIGNMENTS

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22 CCT-2001 (first entry)

Human polynucleotide SEQ ID NO 4959

Human; neetropie; immunosuppressant, cytostatic, gene therapy; cancer; peripheral nervous system, neuropathy, contral nervous system; CMS; Alcheimer(s); Parkinson's disease; Funtington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.

# Homo sapiens.

WO200153312-A1

26-JUL-2001

21 JAN-2000; 26 AFF 2000; 09-JUL-2000; 10 JUL-2000; 03-AUG-2000; 14 SEF-2000; 19-UCT-2000; 27 HTV 2000; 26 DEC-2000; JAN 2000; , 2000US 0488725. , 2000US 0555317. , 2000US 0556317. , 2000US 0600312. 2000US 0653450. 2000US 0668191. 2000US-0693036 2000US-0727344. 2000WO 1834263

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Pred No. 6.8e-136
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The invention relates to human immune system-related protoin and their CC PAA. Human immune-system related precent and ENA are useful for preventing, treating or amelicating a medical condition in a mammalian or subject, for diagnosing preventing or freating liminate cycle. According to disorders, autoimmune disorders (rheumatoid arthritis), inflammatory disorders, autoimmune disorders (rheumatoid arthritis), inflammatory disorders, immune complex failed arthritis), complement afficiency. Inflammatory disorders, immune complex diseases, neoplartic disorders (callergies), infectious diseases (e.g., viral hepatitis), complement afficiency. hyperproliferative disorders (Saucher's disease), disorders (cancer) hyperproliferative disorders (Saucher's disease), disorders (cardiovascular disorders (arrhythmias)) wound healing and epithelial or ell proliferation, endersine disorders (diabetes medition) and complement of the proliferation, endersing hair loss, skin aging due to combine, for maintain organs before transplantation, to treat weight disorders, to physical state, or as a feed additive or preservative. Immune cystem related CNA is useful in June therupy, for thousand June 1 mounts cystem related CNA is useful in June therupy, for thousand and in forensic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Movel isolated immune system related polypoptide useful for treating rheumatoid arthritis, AIDS, allergy, cancer, Gaucher's disease, diabetes rellitus, arthythmia, would health, isohemic lesions and viral hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 300; 315pp; English.
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Best Local Similarity
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                                                                                                                                            Human, open reading frame, OPFX, derection, cytostatic, hepatetropic, vulnerary, antipsoriatic, antiparkinsonian, mostropic, neuroprotective, antipolicant, astempathic, antiparkinsonian, mostropic, neuroprotective, anti-neurolisant, astempathic, antiparkinitic, immunestimulant, thrombolytic, coagulant, vascruppic, antidiabetic, hypotensive, dermatclogical, immunesuppressive, antiinflammatory; hypotensive, dermatclogical, immunesuppressive, antiinflammatory; antithyroid, antithyroid, antisanaemic, gene therapy, cancer, proliferative disorder, hypertension, neurodegenerative disorder, casteearthritis, graft vs host disease; ardiovascular disease, diabetes mellitus, hypothyroidism, SCID, AIDS, cholesterol ester storage, systemic lupus erythematosus; infection, severe rephared immunedisciplicanterial, autoimmune disorder, asthma, allergy, aplastic anaemia, nocturnal haemoglobinuria, burn, wound, borne damage, carrilage damage, antiinflammatory disease, coagulation; this has been damage, carrilage damage, antiinflammatory disease, coagulation;
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Pred No R ne 122;
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Homo sapiens.

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Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allergies, aplastic anaemia, burns, wounds, bone and cartilage damage nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurod-generative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellinus, hypertension, hyperbyroidism, inclessed ester stratege, systemic lup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunostimulant; cardiant; thromboly ic, coagulant; vasotropi antidiabetic; hypotensive; dermatological; immunosuppressive; antifiammatory; antibacterial; antivital; antifundal; antifundal; antificularity;
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                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         ABL68560 standard; DNA; 267156 BP
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CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly or from WIPO at ftp wipo int/published_pot_sequences.
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(HUMA-) HUMAN GENOME

Barash SC, Ruben SM;

WFI; 2001 483426/52.

metastasis Earlie acids enoughing huran immam/hemater into antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and

Disclosure; SEQ ID NO 39360, 3671pp + Sequence Listing; English

AAK54951 to AAK64702 encode the human immuno/haematopoietic antigen (I) arino acid sequences given in AAM82170 to AAK94921 (I) have sylvostatic activity, and can be used in grow therapy and varying pulsatic interests and polymorles rides may be used in the prevention, diagnosis and treatment of dispases associated with inappropriate (I) expression. For example, they may be used to treat discribers associated with decreased expression by rectifying mutations or delections in a patient's genome that affect the activity of (I) by expressing leading the proteins or recomplement the patients own production of (I) Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to proteins and treat immune/haemacopoletic related discusses, uspecially cancers and cancer matastases of happatoprintic during decides. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention,  $N_0 Y^2 4^3 2^3$ .  $N_0 Y^2 4^3 2^3$  and  $N_0 Y^3$ represent sequences used in the exemplification of the prosent invention ESTORMAN LIFE

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cyrostatic, gene therapy, antineoplastic, Wilm's tumour; adenocarcinoma;
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03-OCT-2000; 2000US:237608P.
01-NOV-2000; 2000US:244867P.
91-NOV-2000; 2009US:245084P.
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                                CTGGGAGGCGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGTACTCCAGCCTGGGGTGACA
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ired. No. 9e-45;
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15-MAY-2002

(first entry)

cancer

related gene sequence SEQ ID NO:2751

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stomach;
             Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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n; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
atic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                             AVALON PHARM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 65608 BP;
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## Oesophagus cancer related gene sequence SEQ ID NO.6005 15-MAY-2002 (first entry) ARI.67668 standard; DNA; 65608 BP

Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancero cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocar 13-DEC-2001. 30 MAY-2001; 2001WO-US10838 Homo sapiens ng; prostate; pancreas; carcinoma; antitumour; cancerous; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

C5-JUN-2000; 2000US-209473P

Claim 1;

SEÇ ID

2751; 44pp; English

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Of The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical organization to be tested for anti-neoplastic activity, determining a change in organization of ar least are gene (I) if a signature years set, where (I) or comprises a sequence (S) selected from 8447 sequences (given in ABL6164 or comprises a sequence (S) selected from 8447 sequences (given in ABL6164 or comprises a sequence (S) selected from 8447 sequences (given in ABL6164 or or comprises in indicative of anti-neoplastic activity. (I) has cyrostatic compression is indicative of anti-neoplastic activity. (I) has cyrostatic compression is indicative of anti-neoplastic activity. (I) has cyrostatic continuity and can be used for producing a product which cois the dara or language for product which cois the dara or language for product which cois the dara or language for the chemical correspond to the dara is sufficient to convey the chemical correspond to the agent. M1 can be used in the corresponding of the agent as a solon, breast, stomach, lung, thyroid, co-sophageal, overiam, kidney, proseate or pancreatic cancer.

The description of cancer and convey the chemical concernation of cancer and convey the cancer and c
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                           cardinoma, papillary cardinoma and Wilm's tumour
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Weaver Z;
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The present sequence is one of a large number of 5° ESTs derived from mpNAs encoding secreted proteins. We OFF has yet been conclusively identified within the present sequence. The 5° ESTs were prepared from rotal human FNAs or polyA-FNAs derived from 10° different through EST sequences usually correspond mainly to the 3° untranclated region. The of the mRNA because they are often obtained from obligo-dT primed cDNA indicates. Such ESTs are not well suited for isolating cDNA organized.
                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST. for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65608 BP, 15987 A, 16979 C, 16761 G, 15878 T; 3 other;
                                                                                                                                                                                                                                                        Claim 1, SEQ ID 12590, 71_{\mathrm{PF}} + CD-ROM; English.
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29-JUL-1999; 99JP-0300253
11-JAN 2000, 2000JP-0118776,
02 MAY 2000, 2000JF-0183767
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                                                                                                                                                                                    Primer sets for synthosizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection
                                                                                                                                                                                                                                                                                                                                                        Ota T,
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                         The present invention describes primer sets for
                                                                             Claim 8; SEC ID 16252, 253\eta_{
m P} +
                                                                                                                                                                and/or
                                                                                                                                                                                                                                                                                                                              Ishii S,
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                                                                                                                                                             diagnosis of the abnormality of the proteins encoded by the
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Human reproductive system related antigen DNA SEQ ID NO: 10010.
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                                                                                                                                                                                                                                                                                                                                         17 JAN 2001, LECTWO DECISES
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Best Local
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INFORMATION FOR SEC ID NO: 33:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammallan Ehospholipase An Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION. Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES. 44
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: P4 on IT: Felease #1 0, Version #1
CURRENT AFFLICATION DATA:
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8 888 497 33
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TELECOMMUNICATION INFERNATION
TELEPHONE: 305-527-4498
TELEPHOX: 305-764-4996
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ATTORNEY, AGENT TRECHMATION
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COMPUTER REALVARIE FORM
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TYPE: nucleic acid
STRANDEDNESS: single
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PART CONGRESSION CONTROL CONTR
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) Sequence 33, A
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                                                                                                                                                                                                                                                                                          175-09-362-230-33
                                                                                                                                                                                                              Matches 285; Conservative
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APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jeffrey J.
APPLICANT: Sellhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipaso A2 Monloctide
TITLE OF INVENTION: Sequences and Low Molecular Meight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Supences Having Internal File one Pinding Sites
NUMBER OF SEQUENCES: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Manbo, Peter J.
REGISTRATION HUMBER: 32,264
PEFFPENCE/POCKET NUMBER: IN:
TELECOMMUNICATION INFORMATION:
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ATTOPNEY/AGENT INFOFMATION:
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ADDRESSEE
STREET: 200
CITY: Fort
                                                                                                                                                                                                                            / March 10 4%;
Local Similarity 77.2%;
                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 15328 base pairs
TYPE: nucleic acid
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200 East Broward Poulevard
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Pred. No. 6.9e-45;
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POT US94-07926-33
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GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A
APPLICANT: Sellhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleoride
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Elbosome Einding Sites
TITLE OF INVENTION: Sequences Having Internal Elbosome Einding Sites
                                                                                   Matches 285;
                                                                                                                          Query Match
                                                                                                       1898
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                                                                                                                                                                                             MOLECULE TYPE:
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TELEPHONE: 365 527-2498
TELEFAX: 305-764-4996
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE POCKET NUMBER: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PO comparable

OPERATING SYSTEM: PC-DGS/MS-DGS

SOFTWARE: PatentIn Pelease #1 0, Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Rossell PA
STREET: 200 East Broward Boulevard
SITY: Fort Lauderdale
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S636 PTGFATT TOVVYSTOTTÓVYTTOTYAKANNYTTAÁGAGCAACÁAATAÁGÁAGTGGOTTOTT S695
                                  1666 TTTAATAATOTEGIA EGGAGAAAGGAAAAGGAAAATITTGGAAGAAAAGTGAAGAAGTCATTTA 1725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33301
                                                                              h 10.4%; Similarity 77.2%; 85; Conservative
                                                                                                                                                                                                                             H: 15328 base pairs
nucleic acid
DEDNESS. single
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IBM PC comparit
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                                                                              Score 210.6; DB 5;
Pred. No. 6.9e-45;
0; Mismatches 74;
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                                                                                                                          Length 15328;
                                                                                Indels 10, Gaps
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                                                                      ; MOLECULE TYPE:
; HYPOTHETICAL:
US-08-629-939-5
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UC-08-629-939-5/c
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              Query Match
Best Local Similarity
   Matches 265;
                                                                                                                                                                                                            TELEPHONE: (202) 293-7860
TELEFAX: (202) 293-7860
INDORMATION FOR SEQ ID NO: "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 320 base pairs
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 12-APPIL-19
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAY-ENTIN PENEASE #1 0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER "15/10/670,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kieback, Dirk G.
TITLE OF INVENTION: METHOUS FOR DIAGNOSING AN INCREASED
TITLE OF INVENTION: PISK OF BPEAST OF GVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER PEADABLE FORM:
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                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                                                                                                        TYPE: nucleic acid
STRANDEDNESS. single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                   NAME. KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/LOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
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     Conservative
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N: 435
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                  10.3%,
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Score 208.2; DB 1; Length 327;
Pred. No. 5e-45;
0; Mismafones 48; Impala 4
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1712 AGAAAGTCCATTTAGG TOGGAOG GAIGAGTTAO ATTOGAAGTO WAYA TTTVYGAGG 1771

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RESULT 6
US-08-759-873-5/c
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                                                                                                                          US-08-759-873-5
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A 6612
TELECOMMUNICATION INFORMATION:
TELEPHONE. (202) 293-7660
TELEPHAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHAPACTERISTICS:
LENGTH: 320 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application MS/08759873 Patent No. 5683885
                                                                             Query Match
Best Local
                                                             Matches 265;
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CLASSIFICATION 435
ATTORNEY AGENT INFORMATION.
NAME: KIT, Gordon
PEGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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TITLE GE INVENTIER METHERS FOR DIAMPHONES AN INCREASES FISH
TITLE GE INVENTIER. OF REFART OF OVARIAN ANDER
                                                                                                                                      HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: I
COUNTRY:
ZIP: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER
                                                                          Local Similarity
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(X-1)
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2100 Pennsylvania Avenue, N W , Suite Ano
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                                                             Conservative
                                                                                                                                                                 linear
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                                                                          10.3%, Score L08.1, DB
82.6%; Pred. No. 5e-45;
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Matches 252; Conservative
                      Query Match
10.2%; Score 207.2; DP 4; Length 5835;
Best Local Similarity AF.4%; Fib-1 No. 3.4e-44;
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                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESIGNATION NUMBER: 40,130
PERFERONE/DOCKET NUMBER: 34900
TELEDOMMINICATION INFORMATION:
TELEDHONE: 60 000 000
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APPLICANT: Schuur, Eric
APPLICANT: Henderson, Daniel
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi
REGISTRATION NUMBER: 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 0-
TELEFAX: 706141
                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                             TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER FILING DATE: 02-M
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                                  ; TOPOLOGY:
US 09-033-556-2
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            Query Match
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                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                       ATTORNEY ARRY INFORMATION
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Henderson, Daniel R. APPLICANT: Yu, De Chao
TITLE OF INVENTION: AFENOUSEUS
TITLE OF INVENTION: HETER-L'op-H
                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEC for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                           TELEPHONE: ASO-R13-SAGO
TELEPHONE: ASO-R13-SAGO
                                                                                                                                                                                                              PRIOR APPLICATION DATA APPLICATION NUMBER. FILING DATE:
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                                                                                                              TELEFAX: 01.
Local Cimilarity
                                                      LENGTH: 5335 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                        APPLICATION NUMBER -
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
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Score 207.2, DB 4
Fred No 3 4e 44,
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        5E 4,
           Length 5835
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Sequence 3, Application US/09614495; Patent No. 6436394; GENERAL INFORMATION.
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INFOPMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1018
COMPUTER BEADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEC for Windows Version 2.0b
CURRENT APPLICATION DATA:
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PEGISTPATION NUMBER: 40,130
PEFEPEN'E/NOTHET NUMBER: 44802-20007.00
TELECOMMUNICATION INFORMATION:
TELEPH-NE: 550-81(-550)
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TITLE OF INVENTION: AGENOVIRUS VECTORS SPECIFIC
POR CELLS EXPRESSING ANDROUGH PROPERTY AND MEDIECO
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                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             ATTURNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                            PPICE APPLICATION DATA:
APPLICATION NUMBER: 09/033,333
FILING DATE: <Unknown>
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FILING DATE: 11-Jul-2000
CLASSIFICATION: <Unknown>
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STATE: CA
                                              LENGTH: 5835 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                             STRANDEDNESS: single
                                                                                                                              TELEFAX: 650-494-0792
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SEQ ID NO: 3:
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 SEC 17 NO:
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US-08-380-916-1/c
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Best Local Similarity 82.4%;
Matches 252, Conservative
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                                                                                       TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 2001
REFERENCE/POCKET NUMBER: FP
TELECOMMUNICATION INFORMATION.
TELEPHONE: 415-781-1985
                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 13-UAN-1994
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPTTEE: IRM PC compatible
OPEPATING SYSTEM: PC-DOS/MS-DOS
SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION: Prostrate
MOLECULE TYPE: DNA (genomic)
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                    TOPOLOGY:
                                  STRANDEDNESS
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                            H: 5836 base pairs
nucleid acid
DEDNESC: Single
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Four Embarcardero Center, Suite 3400
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      IELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHAPACTEPISTICS-
LENGTH: 5836 har-
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Best Local Similarity 82.4%;
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ATTOPNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Catherine, Polizzi M
EEGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34
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WENTION: TISSUE SPECIFIC ENHANCER ACTIVE
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PRICK APPLICATION LATA
APPLICATION UNMBER: US 08/180,916
FILING DATE: 10-JAN-1996,
APPLICATION HUMBER: US 09/180,24T
FILING DATE: 13-JAN-1994
ATTORNEY/AGENT INFORMATION
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TELEFAX: 415-494 0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     NAME: Catherine Polici M
REGISTION NUMBER: 40,130
REFERENCE/DOYFET NUMBER: 149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,813,5600
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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TITLE OF INVENTION: TISSHE SPECIFIC EMHANCER ACTIVE
TITLE OF INVENTION: IN PROSTATE
NUMBER OF SEQUENCES. 2
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CITY: Palo Alto
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COMPUTER READABLE FORM:
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                         NAME: Catherine, Polizz: M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 346
TELECOMMUNICATION INFORMATION:
                                                                                                                 CLASSIFICATION: PHIGE APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                             SCHIMAPE: FASTSEQ for Windows Version 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/023,323
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APPLICATION NUMBER:
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TELECOMMUNICATION INFORMATION
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OPERATING SYSTEM: Windows
SOFTWAPE: FastSEO for Windows Version 2 0b
                                                               NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/TWOKET NUMBER: 348
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Pred, No. 3.4e-44;
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Best Local Similarity 82.4%;
Marches 252; Conservative
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LENGTH: 5836 base pairs
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                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/614,495
FILING DATE: 11-Jul-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
OPERIOR APPLICATION DATA:
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4199 -900999900033193077 0778A75008-3671719338833CTGAGGCAGGTGGA 4130
            APPLICATION NUMBER: 09/033,333
FILING DATE: <Unknown>
ATTOPNEY/AGENT INFOPMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ADDRESSEE: MORRISON & FORRSTER
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NAME: Catherine, Polizzi M
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Pred. No. 3.4e-44;
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TOPOLOGY: linear seq 15 No: 2: SEQUENCE DESCRIPTION: SEQ 15 NO: 2: 15: 09 614-495-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 40,130
REFERENTE/OFFICE NUMBER: 84802-20007.00
TELECOMMINICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                        2026 AAAAAA 2031
                                                                                                                                                                                                    3895 AAAAAA 3890
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEX: 706141
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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                       Pred. Not is the number of results predicted by chance to have a score greater than or equal to the source of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                 Pred. No
                                                                                                                                                                                                                                                                                                                     Published Applications NA:*

1: //SHZ_6/[First-dar4]/ [Fubgna/US07_PUBCOMB.seq:*
2: //SHZ_6/[First-dar4]/ [Fubgna/US07_NEW_PUB.seq:*
2: //SHZ_6/[First-dar4]/ [Fubgna/US08_NEW_FUB_seq:*
3: //SHZ_6/[First-dar4]/ [Fubgna/US08_NEW_FUB_seq:*
6: //SHZ_6/[First-dar4]/ [Fubgna/US07_NEW_FUB_seq:*
6: //SHZ_6/[First-dar4]/ [Fubgna/US08_PUBCOMB.seq:*
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10: //SHZ_6/[First-dar4]/ [Fubgna/US09_PUBCOMB.seq:*
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15: //SHZ_6/[First-dar4]/ [Fubgna/US09_PUBCOMB.seq:*
16: //SHZ_6/[First-dar4]/ [Fubgna/US09_PUBCOMB.seq:*
17: //SHZ_6/[First-dar4]/ [Fubgna/US09_PUBCOMB.seq:*
18: //SHZ_6/
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SUMMARIES
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Sequence 1, Appli	03-10-067-514-1	4,	1691139	0.01	2:3	1)	•
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Sequence 2384, Ap	TE THE THE BATT DER4	 	л 0 2 0	10.5	213	17	1
Sequence 9, Appli	US-09-728-552-9	9	1701	10 5	214	. 6	<i>^</i> .
ŠŤ	US-09-764-891-8396	¥	27154	() ()	214.2	7.5	7
Sequence	US-09-764-891-8149	9	31474	10.6	214.8	14	3
authatibas	US-04-418-745A-1	٦	10283	10.6	215.2	1 3	13
Sequence 10010, A	US-09-764-891-10010	9	7566	10.7	217	12	
Sequence 119,	US 09.962-832 119	7	60,000	ر. د م	219:	11	
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Sequence 180	US-09-954-531-180	9	5 5 5 5 5 5 5 5 5 5	0.8	219.2	ç	
Sequence 1,	US-09-263-959-1	10	684973	8 O.	220	x	
Sequence 7, Appli	US-09-949-842-7	9	1015	25.5	518.2	7	
Sequence 6, Appl	118-00-000-557-5	10	1408	34 9	709 6	2/	
Sequence 4, Appl	115-04-998-557-4		765	37.7	765	ۍ	
Sequence 1077, Ap	US-10-037-270-1077	9	1236	51.1	1037.6	4	
Sequence 3, Appl:	US-09-998-667-3	10	1620	79.8	1620	ų.	
Sequence 5, Appl	US-04-448-557-5	·:-	441.	Š	1830 H	Ŋ	
Sequence	Us-09-998-667-2	10	2031	100.0	2031	_	
Description	10	!	Match Length DB	Match	Score	. NO	

Result

Query

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Sequence 1, Appli	Sequence 3897, <b>А</b> ј	Sequence 7354, Ap.	Sequence 7415, Ap	sequen~- €508, Ap	Seguence 295, App	Sequenc⊬ 1377, Ap	Sequence 1377, Ap	Sequence 1377, Ap	sequence 2355, Ap	Seguence 2355, Ap.	sequence 3, Appli	e-quence 2266, Ap	Sequence 1744, Ap	Sequence 1744, Ap	Sequence 3785, Ap	Sequence 18, Appl	Sequence 642, App	Conguesta et 2012, Ap.	Seguence 7470, Ap	Sequence 1167, Ap	Sequence 1167, Ap	sequence 112, Aff	Primence 112, App.	Sequence 15, Appl	Sequence 749, App

## ALIGNMENTS

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APPLICANT: Masuda, Esteban
APPLICANT: Liao, X. Charlene
APPLICANT: Liao, H. Charlene
APPLICANT: Chu, Peter
APPLICANT: Chu, Peter
APPLICANT: Pardo, Jorge
APPLICANT: Pigel Phintale Liada, Indeporated
APPLICANT: Pigel Phintale Liada, Indeporated
TITLE OF INVENTION TEAT: Middle Liab (1971) hopy
91156 FEFER METER COLUMBER US/09/998,667
CURRENT APPLICATION NUMBER: US/09/998,667
PRIOR APPLICATION NUMBER: US/09/998,667
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                   FEATURE:

FEATURE:

FEATURE:

FAME/KEY: CDS

LUCATION: (498)...(1196)

OTHER INFORMATION: TRAC1

US-09-998-667-2
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US 97 398 567-2
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: 1
SEQ ID NO 2
                                                                                                                                                  Query Match 100 0%; Score 20%); [Pest Local Similarity 100.0%; Fred. No. 0; Matches 2031; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
2031
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US-09-998-667-5

| Sequence 5, Application US/09998667
| Sequence 1 No. US20020146747A1
| GENERAL INFORMATION:
| APPLICANT: Masuda, Esteban
| APPLICANT: Liao, X. Charlene
| APPLICANT: Zhao, Haoran
| APPLICANT: Chu, Peter
| APPLICANT: Pardo, Jorge
| APPLICANT: Pardo, Jorge
| APPLICANT: Rigel Pharmaceuticals, Incorporated
| APPLICANT: Rigel Pharmaceuticals, Incorporated
| TITLE OF INVENTION: TRACI: Medulators of Lymphocyte Activation
| FILE PEFEFENCE: 021044-000600US
| CUEPENT APPLICATION NUMBER: US/04/948,667
| CUEPENT APPLICATION NUMBER: US/04/982,432
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Sequence 3, Application US/09998667

Patent No. US20020146747A1

GENERAL INFORMATION.

APPLICANT: Masuda, Esteban

APPLICANT: Liac, X. Charlene

APPLICANT: Chu, Peter

APPLICANT: Rigel Charmaceuticals, Incorporated

APPLICANT: Rigel Charmaceuticals, Incorporated

ITILE OF INVENTION: TRACT: Modulators of Lymphocyte Activation

FILE REPERENCE, C01044-006600US

CUMPRENT APPLICATION NUMBER: US.60/285,432

PRICE APPLICATION COMBER: US.60/285,432

PRICE APPLICATION ONS: 18
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79 8%, Score 1620, Di
Best Local Similarity 190.0%; Fred. No. 0;
Matches 1620; Conservative 0; Mismatches
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TYPE: DNA
ORGANISM, Home Sagiers
FEATURE:
OTHER_INFOSMATION, human wild type TRAC1 shorter cDNA
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NAME/KEY: CDS
LOCATION: (383) .(1081)
OTHER INFORMATION: TRACT
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US-10-037-270-1077
: S-quence 1077, Application US/10037270
; Publication No. US20030104529A1

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Best Local Similarity
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APPLICANT: Wary, Zhiwei
APPLICANT: Tillinghast, John
APPLICANT: Tillinghast, John
APPLICANT: Drimanac, Radoje T.
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2B
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT APPLICATION NUMBER: 09/52/317
PRIOR APPLICATION NUMBER: 09/52/317
PRIOR APPLICATION NUMBER: 09/52/317
PRIOR FILING DATE: 2000 64 25
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SOFTWARE: [r'_FI_g-n-s V-ision 1 n
SEC_ID NO 1077
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APPLICANT:
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NAME/REY miss featur
LOCATION: (1).I.(1236)

OTHER INCOMMATION: n = 4.1.0 or g
10-037-270-1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/488,725 PRIOR FILING DATE: 2000-01-71
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Ma, Yunging
Man Tompiui
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Zhao, Qing A.
Wehrman, Tom
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ATTOGGACTTOTOAGAAGTACATAGATAAGTATGGACCACTACAAGAACTTGAGGAGACA
                                  KUTI 199A TITI TUTASAKITAKATA JATAK HATBOJAGOA(TAYAA JAAVITTI JAGOAKACA
                                                                                                                                                                                                                                                                                                           TO STATA TOTTO TTO ABAAGSA STOTA BOACTSATGTA SCCAAAAGAATGAAATCA
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Ren, Feiyan
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Yang, Yonghong
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GENERAL INFORMATION:

APPLICANT: Masuda, Esteban

APPLICANT: Liao, Charlene

APPLICANT: Liao, Accharlene

APPLICANT: Chu, Peter

APPLICANT: Pardo, Jorge

AFILICANT: PARD, Jorge

AFILICANT: PARD, Jorge

AFILICANTON NUMBER: US/04/448,667

CURPENT AFFLICATION NUMBER: US/04/448,667

PRIOR APPLICATION NUMBER: US/04/242,432

FELLE FILING DATE: L001-04-06

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1
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GENERAL IMPORMATION:
APPLICANT: Masuda, Esteban
APPLICANT: Masuda, Esteban
APPLICANT: Liac, X. Charlene
APPLICANT: Zhao, Haoran
AFFLICANT: Chu, Feter
APPLICANT: Pardo, Josge
APPLICANT: Pardo, Josge
APPLICANT: Pardo, Josge
APPLICANT: Pigel Phaimaseuticals, Incorporated
ITITES OF INVENTION: TRACT: Modulators of Lymphocyt
FILE REFERENCE. 201044-000600US
CUMPRENT AFFLICATION NUMBER: US 60/282,432
PRIOR FILLING DATE. 2001-04-06
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TYPE: DNA
ORGANISM: Mus sp.
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NAME/KEY: CDS
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LOCATION: (167) .(168)
OTHER INFORMATION: n = a,
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                                                         ATGAGAATCGAAGCAGTTTAGAGAGAATTTAATAAGAAAATTTGGAAGTTAGTAAGACACTT 1080
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                                                                          Marches 520,
                                                                                                                                                                                                                        SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                  ORGANISM: Homo eapters
-09-949-842-7
                                                                                                                                                                                                                                                        FILE REFERENCE: Immune System-Related Polynucleotides, Polypeptides, and Antibodies CURRENT APPLICATION IMPRER U3/03/943,842
CURRENT FILING DATE: 2001 09 02
PRIOR APPLICATION NUMBER- POT/US01/07250
PRIOR FILING CATE 2001-08-07
PRIOR FILING CATE 2001-08-07
PRIOR PRIOR FILING CATE 2000-08-11
PRIOR FILING CATE: 2000-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-949-842-7
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ni et al.
TITLE OF INVENTION: PT047P1
                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver
                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                       LENGTH:
                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOTTATAGTOCATTTAAAAAACTOCTTAATTTTTAATTTTAAAATCTOTTTAACATCCTT 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACLGT@3A@31TTGATGGAAAAGATGTA@TA@3TATTA@TGGTTGTTGTC-----TT_GGGG
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Pred No 8 3e-134;
                                                                                                         DB 3,
                                                                                                         Length 1015,
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                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 822-4900
TELEFAX. (206) 822-631
INFORMATION FOR SEQ ID NO. 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION. SIAGNOSTIC AND THERAFEUTIC COMPOSITIONS AND METHODS WHICH UT:
NUMBER OF SEQUENCES: 1279
                                                                                                                                                                                                                      CLASSIFICATION.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             GURRENT APPLICATION DATA:
APPLICATION NUMBER: Us/
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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ATREET: 6300 Columbia Center,
                                                                                                                                                                PEFERENCE/DOORET NUMBER
                                                                                                                                                                                 PEGISTRATION NUMBER:
                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PO-LUS/MS-LUS
SOFTWARE: Patentim Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                   STRANDEDNESS: single
                                                    LENGTH: 684973 base pairs
                                                                                                                                                                                                       NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 180, Application US/09954531 Putert No. USDC0D0165180A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                    Query Match 10.8%;
Best Local Similarity 80.7%;
                                  Matches 271,
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Weaver, Zoe

TITLE OF INVENTION Fromess for identifying Anni Camer Thetagentic Agents Using :

TITLE OF INVENTION Gone Sets

FILE REFERENCE: 689290-77

CURRENT AFFLICATION MIMBER: US/60/954,531

CURRENT AFFLICATION NUMBER: US/60/233,133

PRIOR AFFLICATION NUMBER: US/60/24,000

PRIOR FILING DATE: 2000-09-18

PRIOR AFFLICATION NUMBER: US/60/24,000

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US/60/234,503

PRIOR APPLICATION NUMBER: US/60/234,503

PRIOR APPLICATION NUMBER: US/60/234,503

PRIOR APPLICATION NUMBER: US/60/234,503

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: US/60/234,503
                                                                                                              OTHER INFORMATION: n=a,t,g or c 09 954-531 180
                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER, US/6
PRIOR FILING DATE: 2000 09 22
NUMBER OF SEQ ID NOS. 1392
                                                                                                                                                      NAME/KEY: misc_feature LOCATION. (1)...(65608
                                                                                                                                                                                           FEATURE.
                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                     LENGTH: 65608
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  1.00 AAAATTITT9GAAGTCAAGAAAGTCCATTTAGGCCGGACGGGTGGCTTACGCTTGTAGTC 1755
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Pred. Ma. 1.2e 48,
0; Mismatches 90;
                                    Scare 219.2, PR 9,
Pred. No. 3.8e-49;
0, Mismatches 58,
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CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
PRIOP APPLICATION NUMBER: US/66/235,082
PRIOP FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/66/234,924
PRIOR PILING DATE: 2000 09-25
NUMBER: US/66/234,924
PRIOR FILING DATE: 2000 09-25
NUMBER: US/66/234,924
PRIOR PILING DATE: 2000 09-25
NUMBER: US/66/234,924
PRIOR PILING DATE: 2000 09-25
NUMBER: US/66/234,924
PRIOR PILING DATE: 300 09-25
NUMBER: US/09-26
SOFTWARDE: Patentin version 3.0
SEC ID NO 292
LENGTH: 65608
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Rest Local Similarity 80 7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: n=a,t,g or consisted 436:292
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FEATURE:
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                     1936 CCGGGAGGCCGAGGTTGCAGTGAGCTGAGATCGCGCCAGTACACTCCAGCCTGGGTAACA 1995
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Pred No. 3.8e-49;
0; Mismatches 58
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RESULT 12
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                                                                                                                            Sequence 10010, Application US/09764891
Publication No. US20030077808A:
GENERAL INFORMATION:
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APPLICANT: EDGEL, Retinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
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APPLICART. Rosen et al.

APPLICART. Rosen et al.

TITLE OF INVENTION UNCleic Acids, Proteins, and Antibodies
FILE PEFERENCE: PC006
CCURRENT AFFLICATION NUMBER: US/09/764,891
CCURRENT FILING DATE. 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEG IF NOS 10231
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FILE REFERENCE: 689290-74

(URREHT AFFLICATION NUMBER 45/59/9452,837

CURRENT FILING DATE: 2001-99-25

PRIOR AFFLICATION HIMBER 45/59/275,977

PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER - US/
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS. 259
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NAME/KEY: misc_feature
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Local Similarity 80.7%;
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Pred, No. 3.8e-49;
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                                                                                                                                                                                                                                                                                      ; TYPE: DNA; ORGANISM: Homo sapiens US-09-938-795A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09938795A Publication No. US20030045688A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.7%,
Best Local Similarity 82.2%,
Matches 264; Conservative
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SEQ ID NO 10010
LENGTH: 7566
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SEQ ID NO 3
                                                                                                                                                                                                                      Matches 272;
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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FRICE APPLICATION NUMBER COSSET, 818
PRICE FILING DATE: 2000-08-25
NUMBER OF SEC ID NOS. 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CHU, CHARLES CHIYUAN
APPLICANT: CHAVAX; SANGEETA S
APPLICANT: MASON, JAMES M.
TITLE OF INVENTION, HOMAN INTERLEVEIN FOUR INCOME FROTEIN
FILE REFERENCE: LIJ-9000-US
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         1824 T95TCTCT9T95AAACTCC9TCTCTACTGAAAATGCCAAAGATT93CTGGACGGG16GC6C6C 1883
                                                                                                 1764 TTGGGAGGCTGAGGCAGGCGGATCACAGGGTCGGGASITCGAGACCAGCCTGGCCAACAC
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                                                                              TTOOGAGGCTGAGGCAGGTGGATCACGAGGTCAGGAGTTCAAGATCAGCCTGGCCAAGAT
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82.9%;
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Fred. No. 3.3e 49;
C, Mismatches EC,
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Pred. No. 1.3e-48;
***cmatches 48;
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US-09-764-891-8396/c
                    GENERAL INFORMATION: APPLICANT: ROSEN et al APPLICANT: ROSEN et al TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE. PC006
CUPPENT APPLICATION NUMBER. US/09/764,891
CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: NUCLEIC ACIDS, Proteins, and Antibodies
FILE REFERENCE: PCOO6
CURPENT AFFILICATION MIMBER US/39/764,891
CURRENT FILING DATE: 2001-01-17
Pric: Application data removed Insent FALM % file wripps
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8149
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Publication No. USZ0030077808A1
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TYPE: DNA
ORGANISM, Homo sapiens
-09-764-891-8149
Prior application data removed - consult PALM or file wrapper
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Bmail: ogaphs-ramail.nih.gov Tissue Procurement: Mikos Palkovits, M.D., Ph.D. cDNA Library Freparation. Michael J. Brownstein (NHOPI), Shiraki Toshiyuki and Piero Carninci (RIKEN) Toshiyuki and Piero Carninci (RIKEN) CNA Library Arrayed by: The I.M.A.G.E. Consortium LLNL DNA Sequencing by: Incyte Genemics, Inc. Clone distribution: MGC clone distribution information can in- found through the I.M.A.G.E. Consortium/LLNL at: found through the I.M.A.G.E. Consortium/LLNL at: Plate ILAMITA9 row a column: 15 Plate ILAMITA9 row a column: 15 Plate ILAMITA9 coquence stop: 749. Location/Qualifiers	Oppredikthed (1999) Oppredit Pobert Strausberg, Ph.D.	NIH MGC DIED//MGC.DC1.D1D.GOV/. National Institutes of Health, Mammallan June Colluction (M):	Eukaryota, Medarda, Chordata, Craniata, Verrebiata, Euter, cetroni, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 o 743)		mRNA sequence. B1666910 B1646910 1 CT:15881143 EST.	Bive8910 743 kp mRNA linear Edi id Seb 2001 603791657E1 NIH_MGC 96 Homo sapiens chNA clone IMAGE,5119998 CV,

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s (hases 1 to 1407)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai,
Arakawa, T., Rajiawa, K., Brono, H., Brownstein, M., Bult, C.,
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.
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Eutheria; Rodentia; Schurognathi, Muridae; Murinae; Mus
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                                                                                                       Arai, A.,
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Query Match       34.4%;       Score 699.6;       DB 11;       Length 1407;         Best 10:41 0:mlatity 75 7%;       Prod No. 4 2e-11;       Matches 1029;       Gaps 12;         Matches 1029;       Conservative 0;       Mismatches 301;       Indels 30;       Gaps 12;         Oy       373 GCTGGGGGGAGATTTP9FAMPUTPSTAPETPSTAPETPSTAMTTPCTTPCTTCCTCCCGGGGGGG       432         I       IIII       IIII       IIII       IIII       IIII       IIII       IIIII       IIII       IIIII       IIIII       IIIII       IIII       IIIII       IIIII       IIIII       IIIII       IIIII       IIIIII       IIIIIII       IIIIIIIII       IIIIIIIIIIIII       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	/protein_id="BAB30115.1" /protein_id="BAB30115.1" /db_xief="G1-12854713" /db_xief="G1-12854713" /db_xref="G1-12854713" /db_xref="G1-12854713" /db_xref="G1-12854713" /translation="APAPPALHREADPPGMPSGEAAIPPGGMCGMCLEVUHQD SSWQLAEDERKXIDAREADGACAVARLEHPADSGAFAIPPGGMCGMCLEVUHQD SSWQLAEDERKXIDAREAGACAVARLEHPADSGAFAIPPGGMCSECLEVUHQD SSWGMAHIPTGEKYIDKYGDLEIGATTAACCVCPPCQREDDEDCLIDHCIIHHR GERPVEGENTT" SERPVEGENTT" SERPVEGENTT" SALEYVNOSNTT" BASE "GUNT 377 a 348 g 344 t 2 others	/db xref="RANIOM HH-749055F04" /db_xref="MGD:MGTI1897414" /db_xref="MGD:MGTI1897414" /db_xref="MGD:MGTI1897414" /dbx="male" /sex="male" /tissue_type="testis" /tissue_type="testis" /tissue_type="testis" /tissue_type="testis" /tissue_type="destis" /tissue_type="destis" /tissue_type="destis" /tissue_type="testis" /tissue_type="test	GARACHRONG ANTENNATION TRANSPORTED ST. CONA was cleaved with PamHI and XhoI. Vector: a modified pBluescript RS(+) after bulk excision from Lambda FLC I Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B. end: BamHI. Host: DH10B. Invarion/Qualifiers 1. 1407 2. 1407 2. 1407 2. 1407 2. Strain="C57BL/60"	Please visit our web site (http://genome gsc riken go.jp/) for further details cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Pescarch Group in Piken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Sivision of Experimental Animal Pescarch in Piken contributed to prepare mouse tissues. First strand CDNA was primed with a primer [5' 3AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	Hara A. Hayarsu,N. Hill,D. Hiramoto,K. Hiraoka,T., Hori,F., Hume,D. Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Karo H., Kawai, T., Kojima,Y., Konno,H., Souda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Mishi,K., Momura,K., Numaraki,P., Ohno,M., Okazaki,Y., Shida,K., Sano,H., Sasaki,D., Salto,H., Salbata,K., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Sakai,K., Sano,H., Sasaki,D., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamuta,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayachizaki,Y Direct Submission Submitted (10-SUL-2003) Yushihide Hayashizaki, The Institute of Physical and Chemical Pessarch (PIKEN), Laboratory for Genome Exploration Pessarch (FIKEN), Laboratory for Genome Exploration Pessarch (FIKEN), Laboratory Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Oxohama, Kanagawa 20-0045, Japan (F-mail-genome-resuger riken.go.jp, URLibtp://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
OY 1490 GASATTOTTACACATCTAACAACAAAAAATTATCTACATCAGTCAGT	AAGGGAAAAGGGACCACTGAATTGCACCATTTAAGATGCTGCTTGAACAAATAGGT	OY 1150 TAGACCGTCACTTCTGAATATATATATATATATATATATA	SICAGAGGGAACIGIATIGAAGACAGCITGCTGGATCATTGTA 96	ATCTTCCTTCAGAAGGAGTTCCAGACTGATGTAGCCAAAAAGAATGAAATAAAT	Oy  433 GGCAACAAAACAAACCTTSCGGAAGACCAAACAAGTAGACGTTATTAGACAAGTTAGACGATTAGACAAGACAAAACAAGACAAGACAAGACAAGACAAAACAAGAAAAAA

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RESULT 3
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57, mBMA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Plate: LLAM12351 row: b column: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement, ATCC
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1 (bases 1 to 1086)
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   Email: cgapbs-r@mail.nih.gov
                                    Contact: Pobert Strausberg, Ph.D
                                                          Unpublished (1999)
                                                                                      National Institutes of Health, Mammalian
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Rawal, J., Shinagawa, A., Shibara, F., Yoshino, M., Itoh, M., Alaihi, T., Harl, A., Fikhnishi, Y., Edd., H., Alaihi, T., Fikhda, S., Alzawa, K., Irawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Caravi, Y., Cojiri, T., Finth R., Raybawa, T., Caravi, Y., Cojiri, T., Finth R., Raybawa, T., Caravi, Y., Casavant, T., Fleischmann, W., Gaasterland, T., Gisei, C., King, B., Kochiwa, H., Kuchi, P., Lewis, S., Matsov, Y., Nikado, I., Pesole, G., Yuackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Firmno, M., Aono, H., Wagner, L., Washio, T., Sakai, K., Okido, T., Firmno, M., Aono, H., Baldarelli, R., Barnb, G., Blake, J., Beffelli, P., Bojita, M., Saribodi, M., Guysincieb, S., Hilli, T., Mombert, C., Fijita, M., Saribodi, M., Guysincieb, S., Hilli, T., Mombert, P., Marchionni, L., Mashima, J., Marcarelli, J., Momberts, P., Mordoup, P., Ping, P., Ping, P., Ping, P., Pingwald, M., Rodriguer, I., Sakamoto, N., Sayaki, H., F., Saro, Y., Schrobech, S., Hasegawa, Y., Eawaji, H., Editsuki, S. and Hayashizaki, Y., Oshida, K., Hasegawa, Y., Eawaji, H., Editsuki, S. and Hayashizaki, Y., Sakai, K., Kasi, K., Marcarelli, J., Momberts, M., Finctioni, J., Kasi, K., Hasegawa, Y., Eawaji, H., Editsuki, S. and Hayashizaki, Y., Sakai, K., Kasi, K., Hasegawa, Y., Eawaji, H., Editsuki, S. and Hayashizaki, Y., Sakai, K., Kasi, K.
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High efficiency full length oDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/translation="MDMSILPAYLESEPVPATD!AKEMKSEYQWCAECGTLVCLSDME
AHIPTCEKYIDKYGPLLEIGDTTARCVCPECQPELDEDCLLDHCTIHHESERPEVECP
                                                                                                                                                                                                                                                                                                                     /protein_id="BAB24656.1"
/db_xref="G1.12829739"
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                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
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                                                                                                                                                                                                     | 1117 | ATATAATTIAN NAANCUSTEKKTOONAN INSTELTIASKE SASISCALTEETTINAATATSIFIN | 1178 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 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CO1277726F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE-3618390
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National Institutes of Health, Mammalian Gene
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1 (bases 1 to 627)
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GRACTACTACAAGAACTTRAAGAACAACAGCAAGCTGTGTGTATGTCCCTTTTTGTCAGAAGG
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                                                         AATCACTCGAACACACATAATTTTATTAAAACGAAGGGAAAGGGAACCACTGAATTGCA
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/clone=lika="NIH MGC 20"
/tissue_type="melanotic melanoma"
/lab host="DH10B (phage-resistant)"
/n:t=="Organ skin, Vertor gCTB7, Site 1: Xho1, Site 2:
/n:t=="Organ skin, Vertor gCTB7, Site 1: Xho1, Site 2:
/n:t=="Organ skin, Vertor gCTB7, Site 1: Xho1, Site 2:
/n:t=="Organ skin, Vertor gCTB7, Site 1: Xho1, Site 2:
/n:t=="Organ skin, Vertor gCTB7, Site 1: Xho1, Site 2: Cloned into EcoRI/Xho1 sites using the following 5'
cloned into EcoRI/Xho1 sites using the following 5'
adaptor: GCCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
81 a 129 c 145 g 171 t 1 others
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/db_xref="taxon:9606"
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Tissue Procurement: Lothar Hernighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyre Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate LLM8E?o row : column: 13
High quality sequence stop: 662.
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Contact: Robert Strausberg, Ph.D
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National Institutes of Health, Mammalian
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Mammalia, Eutheria, Rodentia, Sciuregnathi, Muridae, Murinae, Mus
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                                                                                                                                   CGCAACTGACATAGCCAAGAGGATGAAGTCAGAATACCAGAACTGTGCTGAGTGTGGGAAC
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/tissue_type="tumor, gross
/dev_stage="7 months"
/lab_host="D108"
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NIH-Was http://mgc nci nih gev/
National Institutes of Health, Mammalian Gene Collection (MGC)
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Seq primer: -40RP from Gibco
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab host="DH1MB (phage-resistant)"
/lab host="DH1MB (phage-resistant)"
/lab host="Cryan: skin, Vector porBr), Sire_: XhoI, Sire_2
/note="Cryan: skin, Vector porBr), Sire_: NhoI, Sire_2
/note="Cryan: skin, Vector porBr)
// cloned into EcoRI/XhoI sites using the following 5'
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G) Size-selected >500bp for average
insert size 1.8kb Libtary constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                High quality sequence stop: 764.
Location/Qualifiers
                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image llnl gov Flate. LLAM11804 row f column: 20
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
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/clone_lib "NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
                                                                           /clone="IMAGE:5317267"
                                                                                                        /strain="129,C57BL/6J,EVB/N"
/db xref="taxon:10090"
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Contact: Pobert Strausberg, Ph
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Contact. Robert Strausberg, Ph.D.
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Clone distribution: MGC clone distribution information can be found through the I M A G E Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGCCATTATTOGOAGGAGGTTAAGACOGTTCACTTGAATA 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGGTGTTAT---GGGAAGAGTGTTAGAGGGTCACTTCTTGAATA 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTTTUULATTUALISALUTSATSAAAGECCAAGTACCTTCAATGGCAGTTTAATTAGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCTTGCTGGATCATTGCATTATCCACCACAGATCAGAAAGGAGGCCCGTGTTCTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CASCITECTATATTATTATTATCATCACAGACEGAACEGAGCCTGTGTTCTCTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVIAGIAGACAGCAGCAAGGTGTGTGTGTCCCCTTTTGTCAGAGGGAACTGTATGAAGA 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATUAGGGCACATATTCGGACTTGTCAGAAGTACATAGATAAGTATGGACCACTAGAAGA PKK
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                                                     246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rgaphs-r@mail nih
                                                                   /note-"Organ. mammary, Vector: pCMV-SFORT6; Site_1. SalI, Site_2. Not1, Cloned unidirectionally. Frimer Oligo dT. Library constructed by Life Technologies. Investors providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                        /dev_stage-"5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Mam4"
/tissue_type="tumor, gross
                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:5293606"
                                                                                                                                                                                                                                                                                                     /strain="NMRI"
                                                                                                                                                                                                                                                                                                                       organism "Mus musculus"
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14
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Score 399.2;
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Mus musculus cDNA clone (MAGE-5293606 5),
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1621 AGAAATOTGCTCCAATGCTOTTGTTCTAATCTCTAATAGG 1660
                                                                                                                                                                                                                                                                                                                                                                                 1441 TACATOGAAAAGACAOGTOGTAOGCAAGTAGGTOGAVSAVCTCGGTTTGCAAATTAGATA 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1201 ATTAAAAGGAAAAAGGAAAAGTAACTAATTAACATTTAAGATGCTGCTTGAACAA 1260
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                                                                                                                                                                                                                                                                        1501 ATACTCTGTGTATAATGCTACATATCAATAACTACCATCATGGTTAGGGAGGATAACTAA 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1261 TSGGAGGGANGTTGTCAATGATTGATGGGCANAAATGTATAACAACAGTTATGTGTTTTGTC 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                663
                                                                                                                                                                                                                                                                                                                            KAR CAGATOSANGNONAMANGACACNOSCIPSPOTATOTGATGGAGGAGCTICCIBIGICCATIA 698
                                                                                                                                                                                                                                                                                                                                                                                                                                        583 TACATTOTOJAGTOTATTAGACATTTAADUNDGAGAGAGOCTO----TOAGGCATTAA 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 T GGAGGGGGATTGTCGACGTTTGATGGAGAAAAAATGTACTACAGTATTACCTGCTTGTC 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 CACGACCTGATGAAAGCCCAAGTACCTTCAATGGCASTTTAATTAGACATTTGCAAGTCA
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817 TGAAATGT-TTCAAATTCTCATGCTCTATCTCCAATAAGG 855
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                                                                                                                                                            TCTTTSTTCTSTSTAAAAAAAAATATTAASASTJAAAA AAA JIB LAGA AATT AAAGAAATA 1620
                                                                                                                                                                                                                    GTGATGTGTGTATAAACGCTACATATTCCCAACTGTCATCATGTTTAGGGGAGAAAGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCACAC-TTGTTTTATGATGATTTCATAGA-TTTGATAATTGAGGAGGCATTATTC
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                                                                                                           TOTOTOTOCATO--CTAAAAGACGGAAGGAAAGACCAAATATGGACCTTAAAGGAAATC 816
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BB654038 RIKEN full-length enriched, adult male liver tumor Mus musculus cDNA clone C730043K02 5', mRNA sequence.

dq 97.9

mKNA.

linear

BST 16 OCT 1901

EST

house mouse

BB654038.1 GI:16487866

BB654038

BB654038

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FEATURES
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URL:http://genome.gsc.riken.go.jp,
Carninoi,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okaraki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subbraction of cap-trapper-selected cDNAs to
prepare full length cDNA libraries for trapper-selected cDNAs to
prepare. Genome Res. 10 (10), 1617-1630 (2000)
wagi,F., Fujiwako,S., Indue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Indue,Y., Kira,A. and
Hayashizaki,Y.
RYEN integrated sequence analysis (RISA) system 384-format
RYEN integrated sequence analysis (RISA) system 384-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encyclopedia, real time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Fondo S., Shinagawa, A., Saito T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muramatsu, M. and Hayashizaki, Y.
PIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Genome Seguences.
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Tel: 81-45-503-9222
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Shehiro-150, Tsurumi-ku, Yokohama, Kanagawa 230-6045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     further details
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Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 676)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with Numan Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissues.
                                                                                                                                                                                                                                                              Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                           cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                      prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                             contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Site 1 Sall: Site 2 BamHI cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
was cleaved with BamHI and XhoI. Vector: a modified pBluescript\ KS(+) after bulk excision from Lambda F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="liver tumor"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, adult male liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lab_host="DH10B"
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KEYWORDS
SOURCE
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Email: cgapbs-ramail.nih.gov
Tissue Procurement: Dr. James R. Lupski
rDNA Library Preparation: Life Technologies, Inc.
rDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
rDNA Sequencing by. Agencourt Bioscience Colporation
rDNA sequencing by. Agencourt Bioscience Colporation
rDNA carriewing MCC cline distribution information can
found through the L.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D
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                                   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.P. and Adams,M.D.
                                                                                                                      Eukaryota, Mctazoa, Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Eukaryota, Metazoa,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
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/clone_lib="Lupski_dorsal_root_ganglion"
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/db_xref="taxon:9606"
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                               SOURCE
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                                              KEYWORDS
                                                                VERSION
                                                                                                            DEFINITION
              ORGANISM
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Best Local Similarity
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Other_ESTs: TC61253
Contact: Lee, NH
Norway rat.
Rattus norvegicus
Bukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
                                                                                                          BG671440 mRNA linear EST 30 AFR 2001
DRMBRF04 Rat DRG Libiary Pathus nervegious cDNA clone DRMBRF04 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Institute for Genomic Research
9712, Medical Conter Drive, Rockville,
Tel: (301)-838-3529
Fax: (301)-838-0208
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Seq primer: M13-21.
                                                                                             mRNA sequence.
                                                               BG671440 1
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Site_2: NotI"
a 166 c 153 g 91 t
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/db_xref="ATCC (inhost):2042221"
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79.1%;
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©
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Pred. No. 1.2e-43;
0; Mismatches 101;
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1111 ATTITAATATAATTGAGGAAGCTCTTATCCGAAGAGTCTTAGACCGGTC 1159
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Identification of gene expression profile of dorsal root ganglion in the rat peripheral axotomy model of neuropathic pain proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002) 22056133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, F.R.China. Please contact with Zhang Xu (Xu Zhang tion.ac.on) or Han Zejuang (hanzgschge.sh.on)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory of Sensory System
Institute of Neuroscience
320 Yum Yang Poad, Shanghai 200031,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: xu.zhangsion.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: T3
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                                                                                                                                                                                                                                                                                                                                        CONTOGETTESCETCAGTGAAATGAGGGCACATATTOGGACTTGTCAGAAAGTACATAGATA 870
                                                                                                                                                                                                                       AGAGAGAACTGTATGAAGAGCTGGCTGGATCATTGTATTACTCATCACAGATCGGAAC 990
                                                                                                                                                                                                                                                                                                                                                                                                                  CCSCAACTGACATAGCCAAGAGGATGAAGTCAGAATACCAGAACTGTACTGAGTGTGGAA 60
                                       GIGGCAGTITAATTAGACATTTWAAGTCAGCCACACTTNGTTTTACGACGATTTCATAG
                                                                       GCGGCAATTTAATAAGACATCTGCAAGTTAGTCACACTTTGTTTTATGATGATTTCATAG 1110
                                                                                                                                                                                         AGAGAGAACTGGATGAAGAGTGGTTGGTTGGATCATNGTATTATCCACCACAGATCAGAAA
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86 21-64713446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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82.2%;
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Pred. No. 1.
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Swarnh completed: Cone 27, 2003, 15-50-33 Job time: 2640 secs

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